



SEQUENCE LISTING

<110> THASTRUP, Ole
TULLIN, Soren
POULSEN, Lars K
BJORN, Sara P

<120> NOVEL FLUORESCENT PROTEINS

<130> 4614-0140PUS1

<140> US 09/619,310

<141> 2000-07-19

<150> US 08/819,612

<151> 1997-03-17

<150> PCT/DK96/00051

<151> 1996-01-31

<150> DK 1065/95

<151> 1995-09-22

<160> 23

<170> PatentIn version 3.2

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> GFP2 primer directed to A. victoria

<400> 1

tggaataagc tttatgagta aaggagaaga actttt

36

<210> 2

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> GFP-1 primer directed to A. victoria

<400> 2

aagaattcgg atccctttag tgtcaattgg aagtct

36

<210> 3

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' PCR primer incorporating the Y66H substitution responsible for changing green fluorescence into blue fluorescence

<400> 3
ctacctgttc catggccaac gcttgctact actttcctca tgggtgtcaa tgcttttcta 60
gataccc 67

<210> 4
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' PCR primer incorporating the Y66H substitution responsible for changing green fluorescence into blue fluorescence

<400> 4
aagaattcgg atccctttag tgtcaattgg aagtct 36

<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' primer used to flank the Y66H-GFP

<400> 5
aattggtacc aaggaggtaa gctttatgag 30

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' primer used to flank the Y66H-GFP

<400> 6
ctttcgtttt gaattcggat ccctttagtg 30

<210> 7
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> large NcoI-XbaI vector fragment and ligated to SEQ ID NO:8

<400> 7
catggccaac gcttgctact actctctctt atgggtgttca atgctttt 48

<210> 8
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic NcoI-XbaI DNA linker and ligated to SEQ ID NO:7

<400> 8
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48

<210> 9
<211> 48
<212> DNA
<213> Artificial Sequence

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<223> large NcoI-XbaI vector fragment ligated to SEQ ID NO:10

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48

<210> 10
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> NcoI-XbaI DNA linker ligated to SEQ ID NO:9

<400> 10
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48

<210> 11
<211> 36
<212> DNA
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<220>

<223> 5' primer based on pGFP-N1 plasmid

<400> 11
tggaataagc tttatgagta aaggagaaga actttt

36

<210> 12
<211> 35
<212> DNA
<213> Artificial Sequence

<220>

<223> 3' primer based on pGFP-N1 plasmid

<400> 12
gaatcgtaga tctttatttg tatagttcat ccatg 35

<210> 13
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<212> DNA
<213> Artificial Sequence

<220>
<223> 5' primer based on pZeoSV-LacZ plasmid

<400> 13
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<210> 14
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' primer based on pZeoSV-LacZ plasmid

<400> 14
gcgcgaattc ttattattat ttttgacacc agac 34

<210> 15
<211> 764
<212> DNA
<213> Aequorea Victoria

<220>
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<222> (8)..(721)
<223>

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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
1 5 10

ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt 97
Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
15 20 25 30

gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt 145
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
35 40 45

att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act 193
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
50 55 60

act ttc tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg 241

Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met		
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Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln		
	80					85				90							
gaa	aga	act	ata	ttt	tac	aaa	gat	gac	ggg	aac	tac	aag	aca	cgt	gct	337	
Glu	Arg	Thr	Ile	Phe	Tyr	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala		
95					100					105					110		
gaa	gtc	aag	ttt	gaa	ggt	gat	acc	ctt	ggt	aat	aga	atc	gag	tta	aaa	385	
Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys		
				115					120					125			
ggt	att	gat	ttt	aaa	gaa	gat	gga	aac	att	ctt	gga	cac	aaa	atg	gaa	433	
Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Met	Glu		
			130					135					140				
tac	aac	tat	aac	tca	cat	aat	gta	tac	atc	atg	gca	gac	aaa	cca	aag	481	
Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Pro	Lys		
	145						150					155					
aat	gga	atc	aaa	gtt	aac	ttc	aaa	att	aga	cac	aac	att	aaa	gat	gga	529	
Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Lys	Asp	Gly		
	160					165					170						
agc	gtt	caa	tta	gca	gac	cat	tat	caa	caa	aat	act	cca	att	ggc	gat	577	
Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		
175					180					185					190		
ggc	cct	gtc	ctt	tta	cca	gac	aac	cat	tac	ctg	tcc	acg	caa	tct	gcc	625	
Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala		
				195					200					205			
ctt	tcc	aaa	gat	ccc	aac	gaa	aag	aga	gat	cac	atg	atc	ctt	ctt	gag	673	
Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Ile	Leu	Leu	Glu		
			210					215					220				
ttt	gta	aca	gct	gct	ggg	att	aca	cat	ggc	atg	gat	gaa	cta	tac	aaa	721	
Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys		
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taaatgtcca gacttccaat tgacactaaa gggatccgaa ttc																764	
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<211> 238																	
<212> PRT																	
<213> Aequarea Victoria																	
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Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 17

<211> 764
 <212> DNA
 <213> Aequorea victoria

<220>
 <221> CDS
 <222> (8)..(724)
 <223>

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 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 1 5 10

ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tcc gtt agt 97
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
 15 20 25 30

gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt 145
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 35 40 45

att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act 193
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 50 55 60

act ctc tct cat ggt gtt caa tgc ttt tct aga tac cca gat cat atg 241
 Thr Leu Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 65 70 75

aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag 289
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 80 85 90

gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct 337
 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 95 100 105 110

gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa 385
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 115 120 125

ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa 433
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu
 130 135 140

tac aat tat aac tca cat aat gta tac atc atg gca gac aaa cca aag 481
 Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys
 145 150 155

aat ggc atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga 529
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly
 160 165 170

agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat 577
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp

175	180	185	190	
ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc				625
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala				
	195	200	205	
ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag				673
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu				
	210	215	220	
ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa				721
Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys				
	225	230	235	
taa atgtccagac ttccaattga cactaaaggg atccgaattc				764

<210> 18
 <211> 238
 <212> PRT
 <213> *Aequorea victoria*

<400> 18

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Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn

130		135		140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly				
145		150	155	160
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val				
	165	170		175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro				
	180	185		190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser				
	195	200		205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val				
	210	215	220	
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys				
225	230	235		

<210> 19
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<220>
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ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt	97
Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser	
15 20 25 30	
gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt	145
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe	
35 40 45	
att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act	193
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr	
50 55 60	
act ctc tct tat ggt gtt caa tgc ttt tct aga tac cca gat cat atg	241
Thr Leu Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met	

65	70	75	
aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag			289
Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln			
80	85	90	
gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct			337
Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala			
95	100	105	110
gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa			385
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys			
115	120	125	
ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa			433
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu			
130	135	140	
tac aat tat aac tca cat aat gta tac atc atg gca gac aaa cca aag			481
Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys			
145	150	155	
aat ggc atg gaa tac aat tat aac tca cat aat gta tac atc atg gca			529
Asn Gly Met Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala			
160	165	170	
gac aaa cca aag aat ggc atc aaa gtt aac ttc aaa att aga cac aac			577
Asp Lys Pro Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn			
175	180	185	190
att aaa gat gga agc gtt caa tta gca gac cat tat caa caa aat act			625
Ile Lys Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr			
195	200	205	
cca att ggc gat ggc cct gtc ctt tta cca gac aac cat tac ctg tcc			673
Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser			
210	215	220	
acg caa tct gcc ctt tcc aaa gat ccc aac gaa aag aga gat cac atg			721
Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met			
225	230	235	
atc ctt ctt gag ttt gta aca gct gct ggg att aca cat ggc atg gat			769
Ile Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp			
240	245	250	
gaa cta tac aaa taa atgtccagac ttccaattga cactaaaggg atccgaattc			824
Glu Leu Tyr Lys			
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<210> 20
 <211> 258
 <212> PRT
 <213> Aequorea victoria

<400> 20

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 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
 130 135 140
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
 145 150 155 160
 Met Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys
 165 170 175
 Pro Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys
 180 185 190
 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 195 200 205
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
 210 215 220

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu
 225 230 235 240

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu
 245 250 255

Tyr Lys

<210> 21
 <211> 764
 <212> DNA
 <213> Aequorea victoria

<220>
 <221> CDS
 <222> (8)..(724)
 <223>

<400> 21
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 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 1 5 10
 ctt gtt gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt 97
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser
 15 20 25 30
 gga gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt 145
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 35 40 45
 att tgc act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act 193
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 50 55 60
 act ctc act tat ggt gtt caa tgc ttt tct aga tac cca gat cat atg 241
 Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 65 70 75
 aaa cag cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag 289
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 80 85 90
 gaa aga act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct 337
 Glu Arg Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 95 100 105 110
 gaa gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa 385
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 115 120 125
 ggt att gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa 433

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu
130 135 140

tac aat tat aac tca cat aat gta tac atc atg gca gac aaa cca aag 481
Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys
145 150 155

aat ggc atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga 529
Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly
160 165 170

agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat 577
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
175 180 185 190

ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc 625
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
195 200 205

ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag 673
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu
210 215 220

ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa 721
Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

taa atgtccagac ttccaattga cactaaaggg atccgaattc 764

<210> 22
<211> 238
<212> PRT
<213> Aequorea victoria

<400> 22

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 23

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA sequence at the lacZ-promoter GFP fusion point

<400> 23

aggaaagctt tatg

14